

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1.-4. (Canceled)

5. (Previously Presented) A method for detecting the presence of lung cancer cells in a biological sample comprising the steps of:

- (a) detecting the level of mRNA expression in the biological sample of two or more cancer-associated markers selected from the group consisting of L762P, L550S, L587S, L984P, L552S, and L763P; and
- (b) comparing the level of mRNA expression detected in the biological sample for each marker to a predetermined cut-off value for each marker;

wherein a detected level of expression above the predetermined cut-off value for one or more markers is indicative of the presence of lung cancer cells in the biological sample.

6. (Previously Presented) A method for detecting the presence of lung cancer cells in a biological sample comprising the steps of:

- (a) detecting the level of mRNA expression in the biological sample of two or more cancer-associated markers selected from the group consisting of L762P, L550S, L587S, and L984P; and
- (b) comparing the level of mRNA expression detected in the biological sample for each marker to a predetermined cut-off value for each marker;

wherein a detected level of expression above the predetermined cut-off value for one or more markers is indicative of the presence of lung cancer cells in the biological sample.

7. (Previously Presented) The method of claim 6, wherein step (a) comprises detecting the level of mRNA expression using a nucleic acid hybridization technique.

8. (Previously Presented) The method of claim 6, wherein step (a) comprises detecting the level of mRNA expression using a nucleic acid amplification method.

9. (Previously Presented) The method of claim 8, wherein step (a) comprises detecting the level of mRNA expression using a nucleic acid amplification method selected from the group consisting of transcription-based amplification, polymerase chain reaction amplification (PCR), ligase chain reaction amplification (LCR), strand displacement amplification (SDA), and nucleic acid sequence based amplification (NASBA).

10. (Previously Presented) The method of claim 6, wherein the L762P cancer-associated marker comprises a nucleic acid sequence set forth in SEQ ID NO: 1 or a nucleic acid sequence encoding an amino acid sequence set forth in SEQ ID NO: 2.

11. (Previously Presented) The method of claim 6, wherein the L550S cancer-associated marker comprises a nucleic acid sequence set forth in SEQ ID NO: 5 or a nucleic acid sequence encoding an amino acid sequence set forth in SEQ ID NO: 6.

12. (Previously Presented) The method of claim 6, wherein the L587S cancer-associated marker comprises a nucleic acid sequence set forth in SEQ ID NO: 26 or a nucleic acid sequence encoding an amino acid sequence set forth in SEQ ID NO: 27.

13. (Previously Presented) The method of claim 6, wherein the L984P cancer-associated marker comprises a nucleic acid sequence set forth in SEQ ID NO: 3 or a nucleic acid sequence encoding an amino acid sequence set forth in SEQ ID NO: 4.

14. (Previously Presented) The method of claim 6, wherein the cancer is a small cell lung cancer or a non-small cell lung cancer.

15. (Previously Presented) The method of claim 6, wherein the biological sample is a sample suspected of containing cancer-associated markers or cancer cells expressing such markers.

16. (Previously Presented) The method of claim 15, wherein the biological sample is selected from the group consisting of a biopsy sample, lavage sample, sputum sample, serum sample, peripheral blood sample, lymph node sample, bone marrow sample, urine sample, and pleural effusion sample.

17.-26. (Canceled)